AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions and listings in the application:

IN THE CLAIMS:

1-16. (Cancelled)

17. (Currently amended) A method of simultaneously detecting or quantifying a plurality of different target nucleic ~~acid~~acids (N1, N2, . . .Nn) each having a predetermined first partial sequence F and a predetermined second partial sequence S [(F1, S1), (F2, S2),... (Fn, Sn)] ~~having a predetermined sequence~~ in a specimen comprising:

(a) preparing ~~a probe A and a probe B~~ probes Aa [Al, A2,... An] and probes Ba [B1, B2, ... Bn] to convert target nucleic acids (Fa, Sa) into flag sequences (D0j, D1k) (a, j and k are arbitrary natural numbers; $a_{max} = n$; j_{max} and $k_{max} \geq n$),

said ~~probe A~~ probes Aa [Al, A2,... An] being [[a]]respective first ~~probe~~ probes each of which has a sequence [[F']]F'a [F'1, F'2, ... F'n] complementary to [[a]]the respective first partial sequence [[F]]Fa [F1, F2,...Fn] of the target nucleic acid Na (N1, N2, . . .Nn) and a binding molecule bound to the sequence [[F']]F'a, and

said ~~probe B~~ probes Ba [B1, B2, ... Bn] being [[a]] respective second ~~probe~~ probes each of which has a sequence [[S']]S'a [S'1, S'2, ...S'n] complementary to [[a]]the respective second partial sequence [[S]]Sa [S1, S2, ...Sn] of the target nucleic acid and a flag bound to the sequence [[S]]S'a, wherein said flag comprises four units SD, D0, D1, and ED, each having a desired sequence, and linked in the form of SD+ D0+ D1+ ED; wherein the flag sequences D0j and D1k are located between SD and ED and a combination of the D0j and D1k (D0j, D1k) being assigned respectively to the target nucleic acids (Fa, Sa); and wherein SD and ED are each primer sequences,

(b) mixing the probes Aa [A1, A2, ... An] and the probes Ba [B1, B2, ... Bn] with specimens containing target nucleic acids (Fa, Sa) [F1, S1), (F1, S1), ... (Fn, Sn)] respectively, thereby hybridizing the first ~~probe A~~ probes Aa [A1, A2, ... An] with the respective first ~~partial sequence F~~ partial sequences Fa [F1, F2,...Fn] of the target nucleic ~~acid~~acids and simultaneously hybridizing the second ~~probe B~~ probes Ba [B1, B2, ... Bn] with the

respective second partial ~~sequence S~~ sequence Sa [S1, S2, …Sn]of the target nucleic ~~acid~~acids ~~by mixing the first probe A, the second probe B, and the specimen~~;

(c) ligating the first ~~probe A~~ probes Aa and the second ~~probe B~~ probes Ba, both being hybridized with the target nucleic ~~acid~~acids (Fa, Sa), thereby obtaining ~~a probe (A+B)~~ probes (Aa+Ba);

(d) binding the ~~binding molecule~~ first binding molecules of probe Aa to ~~a substance which is~~ substances capable of being paired up therewith, thereby recovering the ~~probe (A+B)~~ probes (Aa+Ba);

(e) dissociating the flag sequences (D0j, D1k)~~amplifying the nucleic acids constructing the flag by PCR, thereby performing an encode reaction~~;

(f) amplifying the flag sequences (D0j, D1k) by PCR, wherein the PCR uses a primer to which a marker substance is bound, and thereby obtaining the flag sequences (D0j, D1k) to which the marker substance is bound; and ~~performing transcription of a sequence FL' complementary to the single-stranded flag sequence obtained by the encode reaction by use of two primers one of which is a primer having another binding molecule and the other is a primer having a marker substance, thereby performing a decode reaction.~~

(g) detecting or quantifying the marker substance of the flag sequences (D0j, D1k), thereby detecting or quantifying the target nucleic acids (Fa, Sa) ~~binding said another binding molecule to a substance which is paired up therewith, thereby recovering the nucleic acid molecule obtained by the decode reaction; and~~

~~(h) detecting or quantifying the marker substance, thereby detecting or quantifying the target nucleic acid, wherein two of four units function as primers for PCR amplification~~.

18. (Cancelled)

19. (Currently amended) The method according to claim ~~18~~17, wherein ~~said decode reaction has the following steps~~ step (f) further comprises:

~~(i) subjecting the single-stranded sequence encoded to a PCR using an SD sequence and an ED sequence as primers;~~

~~(ii) allowing a binding molecule bound to the SD sequence to bind to another substance which is paired up with the binding molecule, thereby recovering a PCR product;~~

~~(iii) denaturing the PCR product to obtain a single-stranded PCR product;~~

~~(iv) mixing sequences D1n' labeled and D0n' labeled, thereby hybridizing the single strand with the sequences D1n' and D0n';~~

~~(v) ligating the sequences D1n' to D0n';~~

~~(vi) denaturing the ligated sequence to obtain a single-stranded D1n'-D0n' sequence with the marker substance; and~~

~~(vii) hybridizing the sequences D01-D0n with the single-stranded sequence labeled with maker substance, to detect or quantify the marker substance, thereby detecting or quantifying the target nucleic acid.~~

(f-1) amplifying the flag sequences (D0j, D1k) by PCR,

wherein the PCR uses a primer to which a second binding molecule is bound, and thereby obtains the flag sequences (D0j, D1k) to which the second binding molecule is bound:

(f-2) binding the second binding molecules of the flag sequences (D0j, D1k) to substances capable of being paired up therewith, thereby recovering the flag sequences (D0j, D1k); and

(f-3) amplifying the recovered flag sequences (D0j, D1k) by PCR,

wherein the PCR uses a primer to which a marker substance is bound, and thereby obtains the flag sequences (D0j, D1k) to which the marker substance is bound.

20. (Currently amended) The method according to claim ~~18~~17, wherein ~~the probe B has the sequence S' and a flag comprising three units and bound to the sequence S', where the three units are SD, D0 and ED each having a desired sequence and connected to each other in the form of SD+D0+ED~~ the flag sequence has a three-unit structure consisting of an SD unit, D0j unit and ED unit, and wherein the D0j unit is assigned respectively to the target nucleic acids (Fa, Sa).

21 (Currently amended) The method according to claim ~~18~~17, wherein ~~said step (h) is performed by the sequence D01-D0n immobilized to a DNA capillary~~ step (g) is performed by sequences (D0j, D1k)' complimentary to the flag sequences (D0j, D1k) immobilized to a DNA capillary.

22. (Currently amended) The method according to claim ~~18~~17, wherein, in said step (d), said substance ~~is immobilized to beads such that the probe (A+B) is recovered by binding the probe (A+B) to the beads via the binding molecule~~ capable of being paired up with the first binding molecules are immobilized on beads such that the probes (Aa, Ba) are recovered by binding the probe (Aa, Ba) to the beads via the first binding molecules.

23. (Currently amended) The method according to claim ~~18~~17, wherein said marker substance is a fluorescent substance such that the target nucleic ~~acid is~~ acids are detected or quantified by quantifying the fluorescent substance.

24. (Currently amended) The method according to claim ~~18~~17, wherein each of the units of the flag sequences (D0j, D1k) is an orthonormal nucleotide sequence.

25. (Currently amended) The method according to claim ~~18~~17, wherein said flag sequences (D0j, D1k) ~~is a~~ are double stranded ~~sequence~~sequences.

26-33. (Cancelled)